

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2005, 00:18:59 ; Search time 3598 Seconds
(without alignments)
2578.424 Million cell updates/sec

Title: US-09-982-091A-4

Perfect score: 6836

Sequence: 1 MTGEVGVSEVHLEINDENVIS.....LTMSGAPIPGFRLSPDRHG 1332

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 8443130 segs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-LONGLOG -DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6836	100.0	4756	9	US-09-982-091A-3	Sequence 3, Appli
2	6822	99.8	4804	20	US-10-357-930-30217	Sequence 30217, A
3	2687	39.3	4754	9	US-09-982-091A-1	Sequence 1, Appli
4	2019	29.5	58837	9	US-09-982-091A-5	Sequence 5, Appli
5	850	12.4	511	15	US-10-106-698-1256	Sequence 1256, Ap
6	813	11.9	111206	13	US-10-087-192-1957	Sequence 1957, Ap
7	763	11.2	547	9	US-09-998-598-480	Sequence 480, App
8	697	10.2	5439	24	US-11-097-143-857	Sequence 857, App
9	656	9.6	484	9	US-09-998-598-268	Sequence 268, App
10	635	9.3	496	10	US-09-918-995-21694	Sequence 21694, A
11	610	8.9	421	10	US-09-803-719-1138	Sequence 1138, Ap
12	606	8.9	9315	24	US-11-097-143-856	Sequence 856, App
13	554	8.1	422	10	US-09-803-719-1139	Sequence 1139, Ap
14	544	8.0	452	20	US-10-357-930-45720	Sequence 45720, A
15	523	7.7	401	20	US-10-357-930-15892	Sequence 15892, A
16	508	7.4	393	10	US-09-803-719-853	Sequence 853, App
17	500	7.3	408	10	US-09-803-719-777	Sequence 777, App
18	416	6.1	473	20	US-10-357-930-46021	Sequence 46021, A
19	400.5	5.9	24789	24	US-11-097-143-40201	Sequence 40201, A
20	390	5.7	18506	24	US-10-450-763-16627	Sequence 16627, A
21	388.5	5.7	7568	22	US-10-133-937-37	Sequence 37, Appl
22	388.5	5.7	9161	17	US-10-159-563-37	Sequence 37, Appl
23	388.5	5.7	9161	17	US-10-159-563-37	Sequence 37, Appl
24	388.5	5.7	9220	20	US-10-357-930-24403	Sequence 24403, A
25	388.5	5.7	9220	20	US-10-357-930-25254	Sequence 25254, A
26	388.5	5.7	9416	19	US-10-755-889-614	Sequence 614, App
27	388.5	5.7	9416	21	US-10-489-740-114	Sequence 114, App
28	388.5	5.7	11917	22	US-10-765-700-32	Sequence 32, Appl
29	388.5	5.7	11950	16	US-10-252-157-218	Sequence 218, Appl
30	382.5	5.6	4380	17	US-10-094-466-29	Sequence 29, Appl
31	376.5	5.5	7095	18	US-10-205-331-67	Sequence 67, Appl
32	367	5.4	6607	10	US-09-814-353-19998	Sequence 19998, A
33	367	5.4	6616	20	US-10-357-930-23673	Sequence 23673, A
34	366.5	5.4	5331	9	US-09-764-176-6	Sequence 6, Appli
35	359.5	5.3	5040	17	US-10-369-493-45767	Sequence 45767, A
36	355.5	5.2	4721	24	US-11-097-143-29150	Sequence 29150, A
37	354	5.2	8307	24	US-11-097-143-31982	Sequence 31982, A
38	354	5.2	11597	24	US-10-997-143-31981	Sequence 31981, A
39	353.5	5.2	10330	21	US-10-956-157-426	Sequence 426, App
40	353.5	5.2	10330	22	US-10-934-998-25	Sequence 25, Appl
41	353.5	5.2	10452	11	US-09-968-007A-490	Sequence 490, App
42	353.5	5.2	10452	21	US-10-843-641A-6960	Sequence 6960, Ap
43	353.5	5.2	10452	22	US-10-934-998-50	Sequence 50, Appl
44	353.5	5.2	11167	16	US-10-252-157-188	Sequence 188, App
45	353	5.2	422	20	US-10-357-930-16195	Sequence 16195, A

ALIGNMENTS

RESULT 1
US-09-982-091A-3
; Sequence 3, Application US/09982091A
; Patent No. US20020151030A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: DUNPHY, William
; APPLICANT: KUMAGAI, Akiko
; TITLE OF INVENTION: CLASPIN PROTEINS AND METHODS OF USE THEREOF
; FILE REFERENCE: CIT1320-1
; CURRENT APPLICATION NUMBER: US/09/982, 091A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/241, 246
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 11, 2005, 19:40:24 ; Search time 704 Seconds
(without alignments)
3095.910 Million cell updates/sec

Title: US-09-982-091A-4
Perfect score: 6836
Sequence: 1 MTGEVGEVHLEINDPNVIS.....LTWSGAPIPGFRLSPDPHG 1332

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6792.5	99.4	4756	US-09-949-016-4455	Sequence 4455, Ap
2	1988.5	29.1	53737	US-09-949-016-16197	Sequence 16197, A
C 3	416	6.1	601	US-09-949-016-159256	Sequence 159256,
4	388.5	5.7	7571	US-09-949-016-4366	Sequence 4366, Ap
5	388.5	5.7	8146	US-09-976-594-725	Sequence 725, App
6	388.5	5.7	11917	US-09-566-921-32	Sequence 32, Appl
7	388.5	5.7	101300	US-09-949-016-16108	Sequence 16108, A
8	382	5.6	9551	US-08-056-200-93	Sequence 93, Appl
9	382	5.6	9551	US-08-800-644-93	Sequence 93, Appl
10	376	5.5	11236	US-07-853-913-1	Sequence 1, Appli
11	366.5	5.4	5331	US-09-764-176-6	Sequence 6, Appli
12	350	5.1	6755	US-08-931-999-4	Sequence 4, Appli

13	348	5.1	10300	4	US-09-949-016-636	Sequence 636, App
14	344.5	5.0	8590	4	US-09-949-016-5562	Sequence 5562, Ap
15	341	5.0	38575	4	US-09-949-016-17304	Sequence 17304, A
16	341	5.0	119153	4	US-09-949-016-12378	Sequence 12378, A
17	327	4.8	9626	4	US-09-150-867-2	Sequence 2, Appli
18	313	4.6	8503	4	US-09-620-312D-130	Sequence 130, App
19	312	4.6	5361	3	US-08-973-462-2	Sequence 2, Appli
20	312	4.6	6152	3	US-08-973-462-1	Sequence 1, Appli
21	311.5	4.6	6008	4	US-09-949-016-5058	Sequence 5058, Ap
22	311	4.5	3489	2	US-08-728-323A-1	Sequence 1, Appli
23	311	4.5	3489	3	US-09-298-568-1	Sequence 1, Appli
24	311	4.5	3489	4	US-09-410-399-1	Sequence 1, Appli
25	311	4.5	3489	4	US-09-894-273-1	Sequence 1, Appli
C 26	311	4.5	32207	2	US-08-770-379-20	Sequence 20, Appl
C 27	311	4.5	32207	3	US-08-757-669A-20	Sequence 20, Appl
C 28	311	4.5	32207	3	US-09-230-371A-20	Sequence 20, Appl
C 29	308	4.5	8257	4	US-09-595-684B-30	Sequence 30, Appl
30	307	4.5	6861	4	US-09-949-016-1240	Sequence 1240, Ap
31	307	4.5	6861	4	US-09-949-016-1241	Sequence 1241, Ap
32	307	4.5	6861	4	US-09-949-016-1242	Sequence 1242, Ap
33	306.5	4.5	5883	4	US-09-949-016-5001	Sequence 5001, Ap
34	306	4.5	5661	3	US-08-938-105-2	Sequence 2, Appli
35	305.5	4.5	5574	4	US-09-917-254-40	Sequence 40, Appli
36	303	4.4	6175	4	US-08-875-435B-1	Sequence 1, Appli
37	302.5	4.4	7596	4	US-09-023-655-1463	Sequence 1463, Ap
38	302	4.4	11091	3	US-09-134-001C-2243	Sequence 2243, Ap
39	301	4.4	7585	4	US-09-418-710-22	Sequence 22, Appl
40	301	4.4	7585	4	US-09-839-479-22	Sequence 22, Appl
41	300.5	4.4	5857	4	US-09-220-132-79	Sequence 79, Appl
42	299.5	4.4	6016	4	US-09-949-016-2264	Sequence 2264, Ap
43	299.5	4.4	8560	4	US-09-949-016-1788	Sequence 1788, Ap
44	299.5	4.4	8560	4	US-09-949-016-1789	Sequence 1789, Ap
45	299	4.4	6158	4	US-09-799-451-897	Sequence 897, App

ALIGNMENTS

RESULT 1
US-09-949-016-4455
Sequence 4455, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4455
LENGTH: 4756
TYPE: DNA
ORGANISM: Human
US-09-949-016-4455

Alignment Scores:
Pred. No.: 0
Score: 6792.50
Percent Similarity: 99.63%
Best Local Similarity: 99.63%
Query Match: 99.36%
DB: 4
Gaps: 1

US-09-982-091A-4 (1-1332) x US-09-949-016-4455 (1-4756)
Qy 1 MetThrGlyGluValGlySerGluValHisLeuGluIleAsnAspProaenValIleSer 20

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 11, 2005, 19:39:09 ; Search time 9226 Seconds
(without alignments)
5495.513 Million cell updates/sec

Title: US-09-982-091A-4
Perfect score: 6836
Sequence: 1 MTGSEVGEVHLEINDPNVIS.....LTWGAIPPGFRLSPDPHG 1332

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gse1: *
9: gb_gse2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2101.5	30.7	2063	3	AK053847 Mus muscu
3	1494	21.9	1027	5	BQ072224 AGENCOURT
4	1324	19.4	930	4	BM461846 AGENCOURT
5	1323	19.4	883	5	BU193221 AGENCOURT
6	1302	19.0	823	4	BG469801 AGENCOURT
7	1246	18.2	883	5	BU181027 AGENCOURT
8	1186.5	17.4	929	5	BQ963412 AGENCOURT
9	1135.5	16.6	751	7	CF749459 UI-M-HU0-

10	1133	16.6	694	4	BM676972	BM676972	UI-E-E01-
11	1116.5	16.3	943	4	BF968339	BF968339	602269405
12	1111	16.3	942	2	BE882484	BE882484	601507224
13	1096	16.0	794	7	CF739118	CF739118	UI-M-HD0-
14	1071	15.7	656	5	BU662956	BU662956	CI93f06.2
15	1055	15.4	1166	5	BM907939	BM907939	AGENCOURT
16	1044	15.3	743	7	CF738075	CF738075	UI-M-HD0-
17	1041	15.2	785	7	CN528793	CN528793	UI-M-HQ0-
18	1019	14.9	647	7	BM720876	BM720876	UI-E-E01-
19	1015	14.8	700	7	CK635361	CK635361	UI-M-HN0-
20	1004	14.7	898	5	BQ227287	BQ227287	AGENCOURT
21	1003	14.7	869	5	BP166258	BP166258	BP166258
22	1001	14.6	582	5	BP279746	BP279746	BP279746
23	1001	14.6	583	5	BP279788	BP279788	BP279788
24	999	14.6	786	7	CF737000	CF737000	UI-M-HD0-
25	990	14.5	582	5	BP313518	BP313518	BP313518
26	987.5	14.4	720	6	CD578928	CD578928	UI-M-FY0-
27	961.5	14.1	630	7	CF724962	CF724962	UI-M-GZ0-
28	956	14.0	595	7	CN309667	CN309667	170005326
29	950.5	13.9	691	7	CF748227	CF748227	UI-M-HJ0-
30	910	13.3	786	4	BI853368	BI853368	603379950
31	909	13.3	639	7	CF914774	CF914774	B0969A05-
32	907	13.3	529	4	BM799186	BM799186	K-EST0082
33	896.5	13.1	746	4	BG166364	BG166364	602345596
34	891	13.0	853	7	CR585850	CR585850	CR585850
35	881	12.9	513	4	BM828080	BM828080	K-EST0100
36	876	12.8	615	7	CF172511	CF172511	B0908E12-
37	866	12.7	570	6	CA536822	CA536822	C0239B04-
38	855	12.5	583	5	BP363381	BP363381	BP363381
39	854	12.5	611	7	CF172978	CF172978	B0916H04-
40	835	12.2	621	5	BQ560356	BQ560356	H4063G11-
41	827	12.1	582	5	BP221815	BP221815	BP221815
42	827	12.1	707	7	CN458990	CN458990	UI-M-HN0-
43	822	12.0	494	1	A1569660	A1569660	tn04b07.x
44	817.5	12.0	961	6	CA983046	CA983046	AGENCOURT
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ALIGNMENTS

RESULT 1	BC018670	2075 bp	mRNA	linear	HTC 19-NOV-2003
LOCUS	BC018670				
DEFINITION	Homo sapiens claspin homolog (Xenopus laevis), mRNA (cDNA clone IMAGE:4104653), containing frame-shift errors.				
ACCESSION	BC018670				
VERSION	BC018670.1	GI:17391474			
KEYWORDS	HTC.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				
REFERENCE	1 (bases 1 to 2075)				
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buettow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mulahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.C., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 11, 2005, 18:59:23 ; Search time 1512 Seconds
(without alignments)
5215.010 Million cell updates/sec

Title: US-09-982-091A-4

Perfect score: 6836

Sequence: 1 MTGGEVGEVHLLEINDPNVIS.....LTWGCAPIRGFRRLSFDPHG 1332

Scoring table: BLOSUM62

Xgapop 10.0 ,	Xgapext 0.5
Ygapop 10.0 ,	Ygapext 0.5
Fgapop 6.0 ,	Fgapext 7.0
Delop 6.0 ,	Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09982091@CGN_1_1_1094@runat_11102005_162442_21109 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6836	100.0	4755	6	ABK52611	Abk52611 DNA encod
2	6822	99.8	4804	5	ABV30199	Abv30199 Human pro
3	6812	99.6	4414	10	ADC30694	Adc30694 Human nov
4	2687	39.3	4754	6	ABK52610	Abk52610 DNA encod
5	2019	29.5	58837	6	ABK52612	Abk52612 Human Cla

6	850	12.4	511	4	AAH34164	Aah34164 Human col
7	813	11.9	111206	11	ACN45152	Acn45152 Mouse gen
8	780	11.4	1225	6	ABQ77931	Abq77931 Human mac
9	763	11.2	547	6	ABV87169	Abv87169 Human col
10	697	10.2	5439	4	ABL02411	Ab102411 Drosophil
11	656	9.6	484	6	ABV86957	Abv86957 Human col
12	635	9.3	496	9	ACH34482	Ach34482 Human end
13	610	8.9	421	4	AAS38080	Aas38080 Novel hum
14	606	8.9	9315	4	ABL02410	Ab102410 Drosophil
15	554	8.1	422	4	AAS38081	Aas38081 Novel hum
16	544	8.0	452	5	ABV45701	Abv45701 Human pro
17	536	7.8	411	5	AAF66638	Aaf66638 Novel hum
18	531	7.8	406	5	AAF66639	Aaf66639 Novel hum
19	523	7.7	401	5	ABV15901	Abv15901 Human pro
20	508	7.4	393	4	AAS37795	Aas37795 Novel hum
21	504	7.4	300	2	AAZ12683	Aaz12683 Human gen
22	500	7.3	408	4	AAS37719	Aas37719 Novel hum
23	440	6.4	386	5	AAF64422	Aaf64422 Novel hum
24	419	6.1	381	5	AAF64459	Aaf64459 Novel hum
25	416	6.1	473	5	ABV46002	Abv46002 Human pro
26	401	5.9	298	2	AAZ12714	Aaz12714 Human gen
27	400.5	5.9	24789	4	ABL28640	Ab128640 Drosophil
28	390	5.7	18506	4	ABL05592	Ab105592 Drosophil
29	388.5	5.7	7568	5	AAS80823	Aas80823 DNA encod
30	388.5	5.7	8146	12	ADL12996	Adl12996 Human ste
31	388.5	5.7	9220	5	ABV24414	Abv24414 Human pro
32	388.5	5.7	9220	5	ABV25265	Abv25265 Human pro
33	388.5	5.7	9416	6	ABK83800	Abk83800 Human cdn
34	388.5	5.7	9416	8	ACF34559	Acf34559 Gene enco
35	388.5	5.7	9416	12	ADN05259	Adn05259 Antipsori
36	388.5	5.7	9416	13	ADR14613	Adr14613 Human NF-
37	388.5	5.7	11917	12	ADI61664	Adi61664 Human cdn
38	388.5	5.7	11950	10	ADE53871	Ades53871 Human pro
39	388.5	5.7	11965	10	ADF90735	Adf90735 Human hep
40	388.5	5.7	12004	12	ADN04560	Adn04560 Antipsori
41	382.5	5.6	4380	6	ABS78735	Ab878735 DNA encod
42	382	5.6	9551	2	AAZ22301	Aaz22301 CDNA enco
43	378	5.5	4755	13	ACN37449	Acn37449 Tumour-as
44	376.5	5.5	7095	9	ACF25360	Acf25360 Rat micro
45	376	5.5	5946	2	AAQ28398	Aaq28398 Rat nestl

ALIGNMENTS

RESULT 1	ABK52611	standard; DNA; 4755 BP.
ID	ABK52611	
XX	ABK52611;	
AC		
XX		
DT	27-AUG-2002	(first entry)
XX		
DE	DNA encoding human Claspin protein.	
XX		
KW	Chk1 protein; SQ/TQ motif; isoelectric point; cell cycle progression; ds;	
KW	nuclear localisation signal; DNA replication checkpoint; benign neoplasm;	
KW	cell proliferative disorder; malignant neoplasm; human; claspin; gene.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	misc_feature	1..331
FT		/*tag= a
FT		/note= "Specifically claimed in claim 9"
FT		81..4079
FT	CDS	/*tag= b
FT		/product= "Human Claspin protein"
FT		799..903
FT	misc_feature	/*tag= c
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FT		1232..1543
FT	misc_feature	/*tag= d
FT		/note= "Specifically claimed in claim 9"

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 11, 2005, 19:27:03 ; Search time 13152 Seconds
(without alignments)
4907.417 Million cell updates/sec

Title: US-09-982-091A-4
Perfect score: 6836
Sequence: 1 MTGSEVSEVHLEINDPNVIS.....LTWSGAPIRGFRLSFDPHG 1332

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 segs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09982091/runat_11102005_162442_21118/app_query.fasta_1.1479
-DB=GenEmbl -QFWT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_scs: *
12: gb_ey: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6836	100.0	4756	9 AF297866	AF297866 Homo sapi
2	6822	99.8	4804	6 CQ498350	CQ498350 Sequence
3	4838	70.8	4964	10 BC050848	BC050848 Mus muscu
4	3512	51.4	2187	9 BC038991	BC038991 Homo sapi

5	2687	39.3	4754	5 AF297867	AF297867 Xenopus l
6	2473.5	36.2	111862	2 AL139143	AL139143 Homo sapi
7	2019	29.5	194296	9 AL354864	AL354864 Human DNA
8	1846.5	27.0	1093	6 CQ727305	CQ727305 Sequence
9	1618.5	23.7	1751	10 AY324187	AY324187 Mus muscu
10	1079.5	15.8	668	6 CQ727303	CQ727303 Sequence
11	934.5	13.7	213391	10 AL606935	AL606935 Mouse DNA
12	879	12.9	111862	2 AL139143	AL139143 Homo sapi
13	865.5	12.7	223363	2 AC120700	AC120700 Rattus no
14	813	11.9	190338	10 AC129216	AC129216 Mus muscu
15	700	10.2	2230	3 AK174670	AK174670 Ciona int
16	697	10.2	5439	6 CQ573099	CQ573099 Sequence
17	645.5	9.4	343858	2 AC095880	AC095880 Rattus no
18	619	9.1	92047	10 AY135690	AY135690 Mus muscu
19	610	8.9	421	6 AX246208	AX246208 Sequence
20	606	8.9	9315	6 CQ573098	CQ573098 Sequence
21	606	8.9	191335	2 AC010700	AC010700 Drosophil
22	606	8.9	210663	2 AC019525	AC019525 Drosophil
23	606	8.9	315988	3 AE003481	AE003481 Drosophil
24	595	8.7	247462	2 AC134478	AC134478 Rattus no
25	554	8.1	422	6 AX246209	AX246209 Sequence
26	549.5	8.0	203980	2 AC134058	AC134058 Rattus no
27	544	8.0	452	6 CQ513853	CQ513853 Sequence
28	536	7.8	411	6 AX071923	AX071923 Sequence
29	531	7.8	406	6 AX071923	AX071923 Sequence
30	523	7.7	401	6 CQ484025	CQ484025 Sequence
31	523	7.7	1044	5 CR761574	CR761574 Xenopus t
32	508	7.4	393	6 AX245923	AX245923 Sequence
33	504	7.4	300	6 BD212010	BD212010 Novel hum
34	500	7.3	408	6 AX245847	AX245847 Sequence
35	497	7.3	418	9 BC062215	BC062215 Homo sapi
36	487.5	7.1	160827	3 AC009025	AC009025 Drosophil
37	487.5	7.1	193262	3 AC007579	AC007579 Drosophil
38	487.5	7.1	260367	3 AE003808	AE003808 Drosophil
39	454	6.6	73391	8 AP002057	AP002057 Arabidops
40	448	6.6	2243	9 AY113649	AY113649 Drosophil
41	447	6.5	206454	3 AC018737	AC018737 Homo sapi
42	440	6.4	386	6 AX069706	AX069706 Sequence
43	432	6.3	179145	9 AC009785	AC009785 Homo sapi
44	431	6.3	68727	3 AC004516	AC004516 Drosophil
45	428.5	6.3	71023	2 AC004426	AC004426 Drosophil

ALIGNMENTS

RESULT 1	AF297866	4756 bp	mRNA	linear	PRI 21-OCT-2000
LOCUS	AF297866				
DEFINITION	Homo sapiens Hu-Claspin mRNA, complete cds.				
ACCESSION	AF297866				
VERSION	AF297866.1	GI:10944333			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 4756)				
TITLE	Kumagai, A. and Dunphy, W.G.				
JOURNAL	Claspin, a novel protein required for the activation of Chk1 during a DNA replication checkpoint response in Xenopus egg extracts				
MEDLINE	Mol. Cell 6 (4), 839-849 (2000)				
PUBMED	21000493				
REFERENCE	2 (bases 1 to 4756)				
AUTHORS	Kumagai, A. and Dunphy, W.G.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-AUG-2000) Biology, California Institute of Technology, 1200 E. California Blvd., Pasadena, CA 91125, USA				
FEATURES	Location/Qualifiers				
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	/db_xref="taxon:9606"				